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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/759,803

DATE: 09/17/2004

TIME: 09:07:36

Input Set : N:\CrF3\RULE60\10759803.raw.txt

Output Set: N:\CRF4\09172004\J759803.raw

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1 <110> APPLICANT: AFAR, Daniel E. H.
2   HUBERT, Rene S.
3   LEONG, Kahan
4   RAITANO, Arthur B.
5   SAFFRAN, Douglas C.
6 <120> TITLE OF INVENTION: NOVEL PROSTATE-RESTRICTED GENE EXPRESSED
7   IN PROSTATE CANCER
8 <130> FILE REFERENCE: 129.13USU1
9 <140> CURRENT APPLICATION NUMBER: US/10/759,803
10 <141> CURRENT FILING DATE: 2004-01-16
11 <150> PRIOR APPLICATION NUMBER: US/09/547,788
12 <151> PRIOR FILING DATE: 2000-04-12
14 <150> PRIOR APPLICATION NUMBER: US 60/128,860
15 <151> PRIOR FILING DATE: 1999-04-12
16 <160> NUMBER OF SEQ ID NOS: 30
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3051
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapien
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (163)...(1365)
26 <400> SEQUENCE: 1
27   gacgcgtggg cgcgaggcg ctgggcgcac ggcgcgaggc cggccggagc tcgaggccgg      60
28   cggcgggcggg agagcgaccc gggcgggcctc gtagcggggc cccggatccc cgagtggcgg      120
29   ccggagcctc gaaaagagat tctcagcgct gattttgaga tg atg ggc ttg gga      174
30                                     Met Gly Leu Gly
31                                     1
32   aac ggg cgt cgc agc atg aag tcg ccg ccc ctc gtg ctg gcc gcc ctg      222
33   Asn Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val Leu Ala Ala Leu
34   5          10          15          20
35   gtg gcc tgc atc atc gtc ttg ggc ttc aac tac tgg att gcg agc tcc      270
36   Val Ala Cys Ile Ile Val Leu Gly Phe Asn Tyr Trp Ile Ala Ser Ser
37   25          30          35
38   cgg agc gtg gac ctc cag aca cgg atc atg gag ctg gaa ggc agg gtc      318
39   Arg Ser Val Asp Leu Gln Thr Arg Ile Met Glu Leu Glu Gly Arg Val
40   40          45          50
41   cgc agg gcg gct gca gag aga ggc gcc gtg gag ctg aag aag aac gag      366
42   Arg Arg Ala Ala Ala Glu Arg Gly Ala Val Glu Leu Lys Lys Asn Glu
43   55          60          65
44   ttc cag gga gag ctg gag aag cag cgg gag cag ctt gac aaa atc cag      414
45   Phe Gln Gly Glu Leu Glu Lys Gln Arg Glu Gln Leu Asp Lys Ile Gln

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46	70	75	80	
47	tcc agc cac aac ttc	cag ctg gag agc gtc	aac aag ctg tac cag gac	462
48	Ser Ser His Asn Phe	Gln Leu Glu Ser Val	Asn Lys Leu Tyr Gln Asp	
49	85	90	95	100
50	gaa aag gcg gtt ttg	gtg aat aac atc acc	aca ggt gag agg ctc atc	510
51	Glu Lys Ala Val	Leu Val Asn Asn Ile	Thr Thr Gly Glu Arg Leu Ile	
52		105	110	115
53	cga gtg ctg caa gac	cag tta aag acc ctg	cag agg aat tac ggc agg	558
54	Arg Val Leu Gln Asp	Gln Leu Lys Thr	Leu Gln Arg Asn Tyr Gly Arg	
55		120	125	130
56	ctg cag cag gat gtc	ctc cag ttt cag aag	aac cag acc aac ctg gag	606
57	Leu Gln Gln Asp Val	Leu Gln Phe Gln Lys	Asn Gln Thr Asn Leu Glu	
58		135	140	145
59	agg aag ttc tcc tac	gac ctg agc cag tgc	atc aat cag atg aag gag	654
60	Arg Lys Phe Ser Tyr	Asp Leu Ser Gln Cys	Ile Asn Gln Met Lys Glu	
61	150	155	160	
62	gtg aag gaa cag tgt	gag gag cga ata gaa	gag gtc acc aaa aag ggg	702
63	Val Lys Glu Gln Cys	Glu Glu Arg Ile Glu	Glu Val Thr Lys Lys Gly	
64	165	170	175	180
65	aat gaa gct gta gct	tcc aga gac ctg agt	gaa aac aac gac cag aga	750
66	Asn Glu Ala Val Ala	Ser Arg Asp Leu Ser	Glu Asn Asn Asp Gln Arg	
67		185	190	195
68	cag cag ctc caa gcc	ctc agt gag cct cag	ccc agg ctg cag gca gca	798
69	Gln Gln Leu Gln Ala	Leu Ser Glu Pro Gln	Pro Arg Leu Gln Ala Ala	
70		200	205	210
71	ggc ctg cca cac aca	gag gtg cca caa ggg	aag gga aac gtg ctt ggt	846
72	Gly Leu Pro His Thr	Glu Val Pro Gln Gly	Lys Gly Asn Val Leu Gly	
73		215	220	225
74	aac agc aag tcc cag	aca cca gcc ccc agt	tcc gaa gtg gtt ttg gat	894
75	Asn Ser Lys Ser Gln	Thr Pro Ala Pro Ser	Ser Ser Glu Val Val Leu Asp	
76		230	235	240
77	tca aag aga caa gtt	gag aaa gag gaa acc	aat gag atc cag gtg gtg	942
78	Ser Lys Arg Gln Val	Glu Lys Glu Glu Thr	Asn Glu Ile Gln Val Val	
79		245	250	255
80	aat gag gag cct cag	agg gag cct cag gag	cca ggc cgg gag	990
81	Asn Glu Glu Pro Gln	Arg Asp Arg Leu Pro	Gln Glu Pro Gly Arg Glu	
82		265	270	275
83	cag gtg gtg gaa gac	aga cct gta ggt gga	aga ggc ttc ggg gga gcc	1038
84	Gln Val Val Glu Asp	Arg Pro Val Gly Gly	Arg Gly Phe Gly Gly Ala	
85		280	285	290
86	gga gaa ctg ggc cag	acc cca cag gtg cag	gct gcc ctg tca gtg agc	1086
87	Gly Glu Leu Gly Gln	Thr Pro Gln Val Gln	Ala Ala Leu Ser Val Ser	
88		295	300	305
89	cag gaa aat cca gag	atg gag ggc cct gag	cga gac cag ctt gtc atc	1134
90	Gln Glu Asn Pro Glu	Met Glu Gly Pro Glu	Arg Asp Gln Leu Val Ile	
91		310	315	320
92	ccc gac gga cag gag	gag gag cag gaa gct	gcc ggg gaa ggg aga aac	1182
93	Pro Asp Gly Gln Glu	Glu Glu Gln Glu Ala	Ala Gly Glu Gly Arg Asn	
94		325	330	335
				340

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95   cag cag aaa ctg aga gga gaa gat gac tac aac atg gat gaa aat gaa      1230
96   Gln Gln Lys Leu Arg Gly Glu Asp Asp Tyr Asn Met Asp Glu Asn Glu
97           345                      350                      355
98   gca gaa tct gag aca gac aag caa gca gcc ctg gca ggg aat gac aga      1278
99   Ala Glu Ser Glu Thr Asp Lys Gln Ala Ala Leu Ala Gly Asn Asp Arg
100          360                      365                      370
101   aac ata gat gtt ttt aat gtt gaa gat cag aaa aga gac acc ata aat      1326
102   Asn Ile Asp Val Phe Asn Val Glu Asp Gln Lys Arg Asp Thr Ile Asn
103          375                      380                      385
104   tta ctt gat cag cgt gaa aag cgg aat cat aca ctc tga attgaactgg      1375
105   Leu Leu Asp Gln Arg Glu Lys Arg Asn His Thr Leu *
106          390                      395                      400
107   aatcacatat ttcacaacag ggccgaagag atgactataa aatgttcatg agggactgaa      1435
108   tactgaaaac tgtgaaatgt actaaataaa atgtacatct gaagatgatt atttgtgaaat      1495
109   tttagtatgc actttgtgta ggaaaaaatg gaatggtctt ttaaacagct tttgggggggt      1555
110   actttggaag tgtctaataa ggtgtcacia tttttggtag taggtatttc gtgagaagtt      1615
111   caacacccaa actggaacat agttctcctt caagtgttgg cgacagcggg gcttcctgat      1675
112   tctggaatat aactttgtgt aaattaacag ccacctatag aagagtccat ctgctgtgaa      1735
113   ggagagacag agaactctgg gttccgctgt cctgtccacg tgctgtacca agtgctggtg      1795
114   ccagcctggt acctgttctc actgaaaagt ctggctaatt ctcttgtgta gtcacttctg      1855
115   attctgacaa tcaatcaatc aatggcctag agcactgact gttaacacaa acgtcactag      1915
116   caaagtagca acagctttaa gtctaaatac aaagctgttc tgtgtgagaa ttttttaaaa      1975
117   ggctacttgt ataataaccc ttgtcatttt taatgtacaa aacgctatta agtggcttag      2035
118   aatttgaaca tttgtggtct ttatttactt tgcttcgtgt gtgggcaaag caacatcttc      2095
119   cctaaatata tattaccaag aaaagcaaga agcagattag gtttttgaca aaacaaacag      2155
120   gccaaaaggg ggctgacctg gagcagagca tggtagagag caaggcatga gagggcaagt      2215
121   ttgttgtgga cagatctgtg cctactttat tactggagta aaagaaaaca aagttcattg      2275
122   atgtcgaagg atatatacag tgttagaat taggactgtt tagaaaaaca ggaatacaat      2335
123   gggtgttttt atcatagtgt acacatttag cttgtggtta atgactcaca aaactgattt      2395
124   taaaatcaag ttaatgtgaa ttttgaat tactacttaa tctaattca caataacaat      2455
125   ggcattaagg tttgacttga gttggttctt agtattattt atggtaaata ggctcttacc      2515
126   acttgcaaat aactggccac atcattaatg actgacttcc cagtaaggct ctctaagggg      2575
127   taagtaggag gatccacagg atttgagatg ctaaggcccc agagatcgtt tgatccaacc      2635
128   ctcttatttt cagaggggaa aatggggcct agaagttaca gagcatctag ctggtgcgct      2695
129   ggcacccctg gctcacaca gactcccag tagctgggac tacaggcaca cagtcactga      2755
130   agcaggccct gtttgcaatt cacgttgcca cctccaactt aaacattctt catatgtgat      2815
131   gtcttagtc actaaggtta aactttccca ccagaaaag gcaacttaga taaaatctta      2875
132   gactacttct atactcttct aagtctctt ccagcctcac tttgagtcct ccttgggggt      2935
133   gataggaatt ttctcttgct ttctcaataa agtctctatt catctcatgt ttaatttgta      2995
134   cgcatagaat tgctgagaaa taaaatgttc tgttcaactt aaaaaaaaaa aaaaaa      3051
136 <210> SEQ ID NO: 2
137 <211> LENGTH: 400
138 <212> TYPE: PRT
139 <213> ORGANISM: Homo sapien
140 <220> FEATURE:
141 <221> NAME/KEY: SIGNAL
142 <222> LOCATION: (1)...(29)
143 <400> SEQUENCE: 2
144   Met Gly Leu Gly Asn Gly Arg Arg Ser Met Lys Ser Pro Pro Leu Val

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145	1	5	10	15
146	Leu	Ala	Ala	Leu
147	20	25	30	
148	Ile	Ala	Ser	Arg
149	35	40	45	
150	Glu	Gly	Arg	Val
151	50	55	60	
152	Lys	Lys	Asn	Glu
153	65	70	75	80
154	Asp	Lys	Ile	Gln
155	85	90	95	
156	Leu	Tyr	Gln	Asp
157	100	105	110	
158	Glu	Arg	Leu	Ile
159	115	120	125	
160	Asn	Tyr	Gly	Arg
161	130	135	140	
162	Thr	Asn	Leu	Glu
163	145	150	155	160
164	Gln	Met	Lys	Glu
165	165	170	175	
166	Thr	Lys	Lys	Gly
167	180	185	190	
168	Asn	Asp	Gln	Arg
169	195	200	205	
170	Leu	Gln	Ala	Ala
171	210	215	220	
172	Asn	Val	Leu	Gly
173	225	230	235	240
174	Val	Val	Leu	Asp
175	245	250	255	
176	Ile	Gln	Val	Val
177	260	265	270	
178	Pro	Gly	Arg	Glu
179	275	280	285	
180	Phe	Gly	Gly	Ala
181	290	295	300	
182	Leu	Ser	Val	Ser
183	305	310	315	320
184	Gln	Leu	Val	Ile
185	325	330	335	
186	Glu	Gly	Arg	Asn
187	340	345	350	
188	Asp	Glu	Asn	Glu
189	355	360	365	
190	Gly	Asn	Asp	Arg
191	370	375	380	
192	Asp	Thr	Ile	Asn
193	385	390	395	400

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195 <210> SEQ ID NO: 3
196 <211> LENGTH: 4
197 <212> TYPE: PRT
198 <213> ORGANISM: Homo sapien
199 <400> SEQUENCE: 3
200 Asn Ile Thr Thr
201 1
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 4
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapien
207 <400> SEQUENCE: 4
208 Asn Gln Thr Asn
209 1
211 <210> SEQ ID NO: 5
212 <211> LENGTH: 4
213 <212> TYPE: PRT
214 <213> ORGANISM: Homo sapien
215 <400> SEQUENCE: 5
216 Asn His Thr Leu
217 1
219 <210> SEQ ID NO: 6
220 <211> LENGTH: 4
221 <212> TYPE: PRT
222 <213> ORGANISM: Homo sapien
223 <400> SEQUENCE: 6
224 Arg Lys Phe Ser
225 1
227 <210> SEQ ID NO: 7
228 <211> LENGTH: 4
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapien
231 <400> SEQUENCE: 7
232 Lys Arg Asp Thr
233 1
235 <210> SEQ ID NO: 8
236 <211> LENGTH: 4
237 <212> TYPE: PRT
238 <213> ORGANISM: Homo sapien
239 <400> SEQUENCE: 8
240 Thr Thr Gly Glu
241 1
243 <210> SEQ ID NO: 9
244 <211> LENGTH: 4
245 <212> TYPE: PRT
246 <213> ORGANISM: Homo sapien
247 <400> SEQUENCE: 9
248 Thr Asn Leu Glu
249 1

VERIFICATION SUMMARY

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